BEST AVAILABLE COPY

```
;  INFORMATION FOR SEQ ID NO:  58:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  4835 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-976-259-58

Alignment Scores:
Pred. No.:                0.00929        Length:          4835
Score:                    108.00         Matches:         59
Percent Similarity:       31.69%         Conservative:    31
Best Local Similarity:    20.77%         Mismatches:      86
Query Match:              6.09%          Indels:          108
DB:                       4              Gaps:            11

US-09-848-852A-3 (1-332) x US-08-976-259-58 (1-4835)

Qy      42 LeuPheGlnGlySerAspLeuGlyMetAlaGluGluAlaGluArgProGlyGluLysAla 61
           ||||||      :::   ||||||:::            |||:::|||
Db    1350 CTATTTTCCCTCGCTCGCCTAGGTATTGTGACGATGTTCGAACAACCGACTTTGGTGAAT 1409

Qy      62 GlyGlnHisSerProLeuArgGluGluHisVal------ThrCysValGlnSerIle--- 78
             :::                 ||||||:::      :::|||   :::   |||
Db    1410 CAAAAGCCACAATTACCTGCATATGAACATATTTTACGTAGCTGTCCCAGAGACATAGAC 1469

Qy      79 LeuAspGluPheLeuGlnThrTyrGlySerLeuIleProLeuSerThrAspGluValVal 98
           |||     |||:::              |||:::||||||   :::|||
Db    1470 CTGCTTGCATTTATAGATGCTGATGAATTTTTATTGCCACTTGAATCGGAT--------- 1520

Qy      99 GluLysLeuGluAspIlePheGlnGlnGluPheSerThrProSerArgLysGlyLeuVal 118
             |||   |||   |||   ::::::|||         |||          :::
Db    1521 ACCAATTTGTCAGATTTTTTTTCTGAAAAGTTTCAGGATGAGAGTGTCAGCGCTATTGCA 1580

Qy     119 LeuGlnLeuIleGlnSerTyrGlnArgMetProGlyAsnAlaMetValArgGlyPheArg 138
           |||
Db    1581 TTG---------------------------------------------------------- 1583

Qy     139 ValAlaTyrLysArgHisValLeuThrMetAspAspLeuGlyThrLeuTyrGlyGlnAsn 158
                                                                  |||
Db    1584 ----------------------------------------------------------AAT 1586

Qy     159 TrpLeuAsn------------------------------------------------------ 161
           |||   |||
Db    1587 TGGGCAAATTTTGGTTCTAGTGGTGAATGGTTTGCTGAAGAGGGGTTGGTTATTGAACGT 1646

Qy     162 --------------AspGlnValMetAsnMetTyrGlyAspLeuValMetAspThrVal 176
                         |||      |||::::::   :::
Db    1647 TTTACCTATCGTGCCCCGCAATCCTTTAACGTTCATCATAACTTCAAAAGCGTGGTCAAA 1706

Qy     177 ProGluLysValHisPhePheAsnSerPhePheTyrAspLysLeuArgThrLysGlyTyr 196
           ||||||:::|||:::   |||::::::      |||     ||||||          |||
Db    1707 CCCGAACGAGTTAACCGCTTTCATAATCCGCATTATGCTGATTTGCGTTATGGTCGATAT 1766

Qy     197 AspGlyValLysArgTrpThrLysAsnValAspIlePheAsnLysGluLeuLeuLeuIle 216
                             :::|||           ::::::|||:::|||
Db    1767 -------------------------ATCGATGCATTGGGTCGTGATTTGATTCTGCAC 1799

Qy     217 ProIleHis--------------LeuGluValHisTrpSerLeuIleSerValAspVal 231
           |||   |||                ||||||   ||||||   :::   |||
Db    1800 CCGAGGCATGGTAATGGGGTTAGTGCTGAAGTGACTTGGAGCGGTGTCAGGGTA------ 1853

Qy     232 ArgArgArgThrIleThrTyrPheAspSerGlnArgThrLeuAsnArgArgCysProLys 251
                                                 |||          |||
Db    1854 ---------------------------------------AATCACTATGCAGTTAAA 1871

Qy     252 His--------------IleAlaLysTyrLeuGlnAlaGluAlaValLysLysAspArg 266
                          :::   |||:::|||:::      |||          :::|||
Db    1872 TCACTTGAGGAATTCTTGTTGGGCAAGCATCTGCGTGGTAGTGCTGCCACTGCTAATCGA 1931

Qy     267 LeuAspPheHisGlnGlyTrpLysGlyTyrPheLysMetAsnValAlaArgGlnAsnAsn 286
           :::                  |||   |||||||||         |||          |||
Db    1932 GTAAAGCAT-----------AAAGATTATTTCAAG---------GCACATGATCGTAAT 1970
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Qy     287 AspSerAspCys 290
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Db    1971 GATGAAGAGTGC 1982

RESULT 2
US-08-375-709-2
; Sequence 2, Application US/08375709
; Patent No. 5683898
;  GENERAL INFORMATION:
;    APPLICANT:  YAZAWA, Kazunaga
;    APPLICANT:  YAMADA, Akiko
;    APPLICANT:  KATO, Seishi
;    APPLICANT:  KONDO, Kiyosi
;    TITLE OF INVENTION:  Gene Coding For Eicosapentaenoic Acid
;    TITLE OF INVENTION:  Synthesizing Enzymes and Process for Production of
;    TITLE OF INVENTION:  Eicosapentaenoic Acid
;    NUMBER OF SEQUENCES:  19
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lardner
;      STREET:  3000 K Street, N.W., Suite 500
;      CITY:  Washington
;      STATE:  D.C.
;      COUNTRY:  USA
;      ZIP:  20007-5109
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/375,709
;      FILING DATE:  20-JAN-1995
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/178,251
;      FILING DATE:  14-MAY-1993
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  JP 4-147945
;      FILING DATE:  15-MAY-1992
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  WEGNER, Harold C.
;      REGISTRATION NUMBER:  25,258
;      REFERENCE/DOCKET NUMBER:  53466/150/AAOK
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (202)672-5300
;      TELEFAX:  (202)672-5399
;      TELEX:  904136
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1983 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  DNA (genomic)
;    ORIGINAL SOURCE:
;      ORGANISM:  Shewanella putrefaciens SCRC-2874 (FERM
;      ORGANISM:  BP-1625)
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  1..1983
;    FEATURE:
;      NAME/KEY:  mat_peptide
;      LOCATION:  1..1983
US-08-375-709-2

Alignment Scores:
Pred. No.:                0.169          Length:          1983
Score:                    93.00          Matches:         75
Percent Similarity:       32.96%         Conservative:    43
Best Local Similarity:    20.95%         Mismatches:      117
Query Match:              5.25%          Indels:          123
DB:                       1              Gaps:            19
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US-09-848-852A-3 (1-332) x US-08-375-709-2 (1-1983)

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Qy       9 GlyThrIleTrp-AlaArgArgGlyAlaHisLeuAlaProProAspAlaSerIleLeuIl 28
Db     537 GGACCACTTTGGCGGAGCTCGCGGTGTTCAAGAGATGTTCCCTGATGTCAAAGTCTACGG 596

Qy      28 eSerAsnValCysSerIleGlyAspHisValAlaGlnGluLeuPheGlnGlySerAspLe 48
Db     597 CTCA----------------GATAACATCACTAAAGAAATTGTCGATGAGAACGTACT 638

Qy      48 uGly-----------MetAlaGluGluAlaGluArgProGlyGluLysAlaGlyGlnHi 64
Db     639 TGCCGGTAACGCCATGAGCCGCCGCGCAGCTTATCAATACGGCGCAACACTGGGCAAACA 698

Qy      64 s----------------------------SerProLeuArgGluGluHisValThrCy 74
Db     699 TGACCACGGTATTGTTGATGCTGCGCTAGGTAAAGGTCTATCAAAAGGTGAAATCACTTA 758

Qy      74 sValGlnSerIleLeuAspGluPheLeuGlnThrTyrGlySerLeuIleProLeuSerTh 94
Db     759 CGTCGCCCCA------GACTACACCTTAAACAGTGAAGGCAAATGGGAAACGCTGACG-- 810

Qy      94 rAspGluValValGluLysLeuGluAspIlePheGlnGlnGluPheSerThr-------- 111
Db     811 ----------ATTGATGGTCTAGAGATGGTGTTTATGGATGCCTCGGGCACCGAAGCTGA 860

Qy     112 ----------------------ProSerArgLysGlyLeuValLeuGlnLeuIleGlnSe 124
Db     861 GTCAGAAATGATCACTTATATTCCCTCTAAAAAAGCGCTCTGGACGGCGGAGCTT---AC 917

Qy     124 rTyrGlnArgMetProGly---------------------------------------- 130
Db     918 CTATCAAGGTATGCACAACATTTATACGCTGCGCGGCGCTAAAGTACGTGATGCGCTCAA 977

Qy     131 ----------------AsnAlaMetValArgGlyPhe-----------ArgValAlaTy 141
Db     978 GTGGTCAAAAGATATCAACGAAATGATCAATGCCTTTGGTCAAGATGTCGAAGTGCTGTT 1037

Qy     141 rLysArgHisVal-----------------------------------------LeuTh 147
Db    1038 TGCCTCGCACTCTGCGCCAGTGTGGGGTAACCAAGCGATCAACGATTTCTTACGCCTACA 1097

Qy     147 rMetAspAspLeuGlyThrLeuTyrGlyGln------AsnTrpLeuAsnAspGlnVal-- 164
Db    1098 GCGTGATAACTACGGCCTAGTGCACAATCAAACCTTGAGACTTGCCAACGATGGTGTCGG 1157

Qy     165 -MetAsnMetTyrGlyAspLeuValMetAspThrValProGluLysValHisPhePheAs 184
Db    1158 TATACAAGATATTGGCGATGCGATTCAAGACACGATTCCAGAGTCTATC---------- 1206

Qy     184 nSerPhePheTyrAspLysLeuArgThrLysGlyTyrAspGlyValLysArgTrpThrLy 204
Db    1207 ----------TACAAGACGTGGCATACCAATGGTTACCACGGCACT------TATAGCCA 1250

Qy     204 sAsnValAsp---IlePheAsnLysGluLeuLeuLeuIleProIleHisLeuGluValHi 223
Db    1251 TAACGCTAAAGCGGTTTATAACAAGTATCTA---------- 1281

Qy     223 sTrpSerLeuIleSerValAspValArgArgArgThrIleThrTyrPheAspSerGlnAr 243
Db    1282 ------------------------------------GGCTACTTCGATATGAACCC 1301

Qy     243 gThrLeuAsnArgArgCysPro------LysHisIleAlaLysTyrLeuGln-------- 258
Db    1302 AGCCAACCTTAATCCGCTGCCAACCAAGCAAGAATCTGCCAAGTTTGTCGAATACATGGG 1361

Qy     259 -------AlaGluAlaValLysLysAspArgLeuAspPheHisGlnGlyTrpLysGlyTy 276
Db    1362 CGGCGCAGATGCCGCAATTAAGCGCGCTAAAGATGATTACGCTCAAGGTGAATACCGCTT 1421

Qy     276 rPhe--------------LysMetAsnValAlaArgGlnAsnAsnAspSer 288
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Db 1422 TGTTGCAACGGCATTAAATAAGGTGGTGATGGCCGAGCCAGAAAATGACTCC 1473

RESULT 3
US-08-752-929-2
; Sequence 2, Application US/08752929
; Patent No. 5798259
; GENERAL INFORMATION:
; APPLICANT: YAZAWA, Kazunaga
; APPLICANT: YAMADA, Akiko
; APPLICANT: KATO, Seishi
; APPLICANT: KONDO, Kiyosi
; TITLE OF INVENTION: Gene Coding for Eicosapentaenoic Acid Synthesizing
; TITLE OF INVENTION: Enzymes and Process for Production of Eiscosapentaenoic
; TITLE OF INVENTION: Acid
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/752,929
; FILING DATE: 20-NOV-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/375,709
; FILING DATE: 20-JAN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/178,251
; FILING DATE: 14-MAY-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 4-147945
; FILING DATE: 15-MAY-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: WEGNER, Harold C.
; REGISTRATION NUMBER: 25,258
; REFERENCE/DOCKET NUMBER: 53466/150/AAOK
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1983 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Shewanella putrefaciens SCRC-2874 (FERM
; ORGANISM: BP-1625)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1983
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 1..1983
US-08-752-929-2

Alignment Scores:

Pred. No.:	0.169	Length:	1983
Score:	93.00	Matches:	75
Percent Similarity:	32.96%	Conservative:	43
Best Local Similarity:	20.95%	Mismatches:	117
Query Match:	5.25%	Indels:	123
DB:	1	Gaps:	19